

SEQUENCE LISTING

<110> Carulli, John P.
 Little, Randall D.
 Recker, Robert R.
 Johnson, Mark L.

<120> High bone mass gene of 11q13.3

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<140> US 09/544,398

<141> 2000-04-05

<150> US 09/229,319

<151> 1999-01-13

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<151> 1998-10-23

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<212> DNA

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Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser	
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Pro Asp Gly Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr	
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Leu Asp Pro Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr	
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Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile	
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Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser
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Thr His Pro Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr
              240                245                250

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Asp Trp Gln Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly	
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aag agg aag gag atc ctg agt gcc ctc tac tca ccc atg gac atc cag	925
Lys Arg Lys Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln	
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Val Leu Ser Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu	
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gac aat ggc ggc tgc tcc cac ctg tgc ctg ctg tcc cca agc gag cct	1021
Asp Asn Gly Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro	
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Phe Tyr Thr Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly	
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Arg Thr Cys Lys Ala Gly Ala Glu Glu Val Leu Leu Ala Arg Arg	
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Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile	
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Val Leu Gln Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp	
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Pro Leu Glu Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile	
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Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn	
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Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu	
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Asn Gly Thr Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro	
450 455 460	
cga gcc atc gca ctg cac ccc gtg atg ggc ctc atg tac tgg aca gac	1501
Arg Ala Ile Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp	
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Trp Gly Glu Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu	
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Arg Arg Val Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala	
495 500 505	
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Leu Asp Leu Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp	

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Lys Ile Glu Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu							
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Glu Asp Lys Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe							
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Ile Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys							
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Val Lys Ala Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met							
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Gly Leu Lys Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys							
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Ala Asp Arg Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His							
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Ala Thr Arg Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met							
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aag acc tgc atc gtg cct gag gcc ttc ttg gtc ttc acc agc aga gcc							2029
Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala							
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gcc atc cac agg atc tcc ctc gag acc aat aac aac gac gtg gcc atc							2077
Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile							
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Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser							
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Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg							
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Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu							
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gac tac ccc gag ggc atg gcc gtt gac tgg atg ggc aag aac ctc tac							2269
Asp Tyr Pro Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr							
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tgg gcc gac act ggg acc aac aga atc gaa gtg gcg cgg ctg gac ggg							2317
Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly							
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Gln Phe Arg Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser							
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ctg gcc ctg gat ccc acc aag ggc tac atc tac tgg acc gag tgg ggc							2413
Leu Ala Leu Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly							
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Gly	Lys	Pro	Arg	Ile	Val	Arg	Ala	Phe	Met	Asp	Gly	Thr	Asn	Cys	Met	
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Thr	Leu	Val	Asp	Lys	Val	Gly	Arg	Ala	Asn	Asp	Leu	Thr	Ile	Asp	Tyr	
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Ala	Asp	Gln	Arg	Leu	Tyr	Trp	Thr	Asp	Leu	Asp	Thr	Asn	Met	Ile	Glu	
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Ser	Ser	Asn	Met	Leu	Gly	Gln	Glu	Arg	Val	Val	Ile	Ala	Asp	Asp	Leu	
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Pro	His	Pro	Phe	Gly	Leu	Thr	Gln	Tyr	Ser	Asp	Tyr	Ile	Tyr	Trp	Thr	
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gac	tgg	aac	ctg	cac	agc	att	gag	cgg	gcc	gac	aag	act	agc	ggc	cgg	2701
Asp	Trp	Asn	Leu	His	Ser	Ile	Glu	Arg	Ala	Asp	Lys	Thr	Ser	Gly	Arg	
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Cys	Gly	Cys	Ala	Ser	His	Tyr	Thr	Leu	Asp	Pro	Ser	Ser	Arg	Asn	Cys	
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Ser	Pro	Pro	Thr	Thr	Phe	Leu	Leu	Phe	Ser	Gln	Lys	Ser	Ala	Ile	Ser	
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cgg	atg	atc	ccg	gac	gac	cag	cac	agc	ccg	gat	ctc	atc	ctg	ccc	ctg	2989
Arg	Met	Ile	Pro	Asp	Asp	Gln	His	Ser	Pro	Asp	Leu	Ile	Leu	Pro	Leu	
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cat	gga	ctg	agg	aac	gtc	aaa	gcc	atc	gac	tat	gac	cca	ctg	gac	aag	3037
His	Gly	Leu	Arg	Asn	Val	Lys	Ala	Ile	Asp	Tyr	Asp	Pro	Leu	Asp	Lys	
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Phe	Ile	Tyr	Trp	Val	Asp	Gly	Arg	Gln	Asn	Ile	Lys	Arg	Ala	Lys	Asp	
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Pro	Asp	Arg	Gln	Pro	His	Asp	Leu	Ser	Ile	Asp	Ile	Tyr	Ser	Arg	Thr	
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Leu	Phe	Trp	Thr	Cys	Glu	Ala	Thr	Asn	Thr	Ile	Asn	Val	His	Arg	Leu	
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Ala His Pro Cys Ala Arg Asp Asn Gly Gly Cys Ser His Ile Cys Ile	
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Gly Cys Pro Val Cys Ser Ala Ala Gln Phe Pro Cys Ala Arg Gly Gln	
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Cys Val Asp Leu Arg Leu Arg Cys Asp Gly Glu Ala Asp Cys Gln Asp	

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Arg Ser Asp Glu Val Asp Cys Asp Ala Ile Cys Leu Pro Asn Gln Phe				
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Phe Pro Asp Cys Ile Asp Gly Ser Asp Glu Leu Met Cys Glu Ile Thr				
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Ile Ala Pro Gly Gly Ser Gln His Gly Pro Phe Thr Gly Ile Ala Cys				
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Val Pro Leu Tyr Asp Arg Asn His Val Thr Gly Ala Ser Ser Ser Ser				
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Ser Ser Ser Thr Lys Ala Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro				
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Pro Ser Pro Ala Thr Asp Pro Ser Leu Tyr Asn Met Asp Met Phe Tyr				
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Ser Ser Asn Ile Pro Ala Thr Ala Arg Pro Tyr Arg Pro Tyr Ile Ile				
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Leu Asn Ser Asp Ser Asp Pro Tyr Pro Pro Pro Pro Thr Pro His Ser				
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Gln Tyr Leu Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu	
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Arg Ser Tyr Phe His Leu Phe Pro Pro Pro Pro Ser Pro Cys Thr Asp	
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Ser Ser	
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Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu Val Asp Ala	
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Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser Pro Asp Gly	
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115 120 125	
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Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr Pro Arg Ile	
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Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile Val Asp Ser	
180 185 190	
Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys	
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225 230 235 240	
Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln	
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Thr	Arg	Ser	Ile	His	Ala	Cys	Asn	Lys	Arg	Thr	Gly	Gly	Lys	Arg	Lys	260	265	270
Glu	Ile	Leu	Ser	Ala	Leu	Tyr	Ser	Pro	Met	Asp	Ile	Gln	Val	Leu	Ser	275	280	285
Gln	Glu	Arg	Gln	Pro	Phe	Phe	His	Thr	Arg	Cys	Glu	Glu	Asp	Asn	Gly	290	295	300
Gly	Trp	Ser	His	Leu	Cys	Leu	Leu	Ser	Pro	Ser	Glu	Pro	Phe	Tyr	Thr	305	310	315
Cys	Ala	Cys	Pro	Thr	Gly	Val	Gln	Met	Gln	Asp	Asn	Gly	Arg	Thr	Cys	325	330	335
Lys	Ala	Gly	Ala	Glu	Glu	Val	Leu	Leu	Ala	Arg	Arg	Thr	Asp	Leu		340	345	350
Arg	Arg	Ile	Ser	Leu	Asp	Thr	Pro	Asp	Phe	Thr	Asp	Ile	Val	Leu	Gln	355	360	365
Val	Asp	Asp	Ile	Arg	His	Ala	Ile	Ala	Ile	Asp	Tyr	Asp	Pro	Leu	Glu	370	375	380
Gly	Tyr	Val	Tyr	Trp	Thr	Asp	Asp	Glu	Val	Arg	Ala	Ile	Arg	Arg	Ala	385	390	395
Tyr	Leu	Asp	Gly	Ser	Gly	Ala	Gln	Thr	Leu	Val	Asn	Thr	Glu	Ile	Asn	405	410	415
Asp	Pro	Asp	Gly	Ile	Ala	Val	Asp	Trp	Val	Ala	Arg	Asn	Leu	Tyr	Trp	420	425	430
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Ser	Arg	Lys	Ile	Leu	Val	Ser	Glu	Asp	Leu	Asp	Glu	Pro	Arg	Ala	Ile	450	455	460
Ala	Leu	His	Pro	Val	Met	Gly	Leu	Met	Tyr	Trp	Thr	Asp	Trp	Gly	Glu	465	470	475
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Gln	Glu	Gly	Lys	Leu	Tyr	Trp	Gly	Asp	Ala	Lys	Thr	Asp	Lys	Ile	Glu	515	520	525
Val	Ile	Asn	Val	Asp	Gly	Thr	Lys	Arg	Arg	Thr	Leu	Leu	Glu	Asp	Lys	530	535	540
Leu	Pro	His	Ile	Phe	Gly	Phe	Thr	Leu	Leu	Gly	Asp	Phe	Ile	Tyr	Trp	545	550	555
Thr	Asp	Trp	Gln	Arg	Arg	Ser	Ile	Glu	Arg	Val	His	Lys	Val	Lys	Ala	565	570	575
Ser	Arg	Asp	Val	Ile	Ile	Asp	Gln	Leu	Pro	Asp	Leu	Met	Gly	Leu	Lys	580	585	590
Ala	Val	Asn	Val	Ala	Lys	Val	Val	Gly	Thr	Asn	Pro	Cys	Ala	Asp	Arg	595	600	605
Asn	Gly	Gly	Cys	Ser	His	Leu	Cys	Phe	Phe	Thr	Pro	His	Ala	Thr	Arg	610	615	620
Cys	Gly	Cys	Pro	Ile	Gly	Leu	Glu	Leu	Leu	Ser	Asp	Met	Lys	Thr	Cys	625	630	635
Ile	Val	Pro	Glu	Ala	Phe	Leu	Val	Phe	Thr	Ser	Arg	Ala	Ala	Ile	His	645	650	655

Arg	Ile	Ser	Leu	Glu	Thr	Asn	Asn	Asn	Asp	Val	Ala	Ile	Pro	Leu	Thr	660	665	670
Gly	Val	Lys	Glu	Ala	Ser	Ala	Leu	Asp	Phe	Asp	Val	Ser	Asn	Asn	His	675	680	685
Ile	Tyr	Trp	Thr	Asp	Val	Ser	Leu	Lys	Asn	Ile	Ser	Arg	Ala	Phe	Met	690	695	700
Asn	Gly	Ser	Ser	Val	Glu	His	Val	Val	Glu	Phe	Gly	Leu	Asp	Tyr	Pro	705	710	715
Glu	Gly	Met	Ala	Val	Asp	Trp	Met	Gly	Lys	Asn	Leu	Tyr	Trp	Ala	Asp	725	730	735
Thr	Gly	Thr	Asn	Arg	Ile	Glu	Val	Ala	Arg	Leu	Asp	Gly	Gln	Phe	Arg	740	745	750
Gln	Val	Leu	Val	Trp	Arg	Asp	Leu	Asp	Asn	Pro	Arg	Ser	Leu	Ala	Leu	755	760	765
Asp	Pro	Thr	Lys	Gly	Tyr	Ile	Tyr	Trp	Thr	Glu	Trp	Gly	Gly	Lys	Pro	770	775	780
Arg	Ile	Val	Arg	Ala	Phe	Met	Asp	Gly	Thr	Asn	Cys	Met	Thr	Leu	Val	785	790	795
Asp	Lys	Val	Gly	Arg	Ala	Asn	Asp	Leu	Thr	Ile	Asp	Tyr	Ala	Asp	Gln	805	810	815
Arg	Leu	Tyr	Trp	Thr	Asp	Leu	Asp	Thr	Asn	Met	Ile	Glu	Ser	Ser	Asn	820	825	830
Met	Leu	Gly	Gln	Glu	Arg	Val	Val	Ile	Ala	Asp	Asp	Leu	Pro	His	Pro	835	840	845
Phe	Gly	Leu	Thr	Gln	Tyr	Ser	Asp	Tyr	Ile	Tyr	Trp	Thr	Asp	Trp	Asn	850	855	860
Leu	His	Ser	Ile	Glu	Arg	Ala	Asp	Lys	Thr	Ser	Gly	Arg	Asn	Arg	Thr	865	870	875
Leu	Ile	Gln	Gly	His	Leu	Asp	Phe	Val	Met	Asp	Ile	Leu	Val	Phe	His	885	890	895
Ser	Ser	Arg	Gln	Asp	Gly	Leu	Asn	Asp	Cys	Met	His	Asn	Asn	Gly	Gln	900	905	910
Cys	Gly	Gln	Leu	Cys	Leu	Ala	Ile	Pro	Gly	Gly	His	Arg	Cys	Gly	Cys	915	920	925
Ala	Ser	His	Tyr	Thr	Leu	Asp	Pro	Ser	Ser	Arg	Asn	Cys	Ser	Pro	Pro	930	935	940
Thr	Thr	Phe	Leu	Leu	Phe	Ser	Gln	Lys	Ser	Ala	Ile	Ser	Arg	Met	Ile	945	950	955
Pro	Asp	Asp	Gln	His	Ser	Pro	Asp	Leu	Ile	Leu	Pro	Leu	His	Gly	Leu	965	970	975
Arg	Asn	Val	Lys	Ala	Ile	Asp	Tyr	Asp	Pro	Leu	Asp	Lys	Phe	Ile	Tyr	980	985	990
Trp	Val	Asp	Gly	Arg	Gln	Asn	Ile	Lys	Arg	Ala	Lys	Asp	Asp	Gly	Thr	995	1000	1005
Gln	Pro	Phe	Val	Leu	Thr	Ser	Leu	Ser	Gln	Gly	Gln	Asn	Pro	Asp	Arg	1010	1015	1020
Gln	Pro	His	Asp	Leu	Ser	Ile	Asp	Ile	Tyr	Ser	Arg	Thr	Leu	Phe	Trp	1025	1030	1035
Thr	Cys	Glu	Ala	Thr	Asn	Thr	Ile	Asn	Val	His	Arg	Leu	Ser	Gly	Glu	1045	1050	1055

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 Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly Leu Glu Asp
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 Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val Tyr Trp Thr
 65 70 75 80
 Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn Gln Thr Gly
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 Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser Pro Asp Gly
 100 105 110
 Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu
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 Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val
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 Leu Phe Trp Gln Asp Leu Asp Gln Pro Lys Ala Ile Ala Leu Asp Pro
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 Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Val Glu Thr Pro Arg Ile
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Glu	Arg	Ala	Gly	Met	Asp	Gly	Ser	Thr	Arg	Lys	Ile	Ile	Val	Asp	Ser	180	185	190
Asp	Ile	Tyr	Trp	Pro	Asn	Gly	Leu	Thr	Ile	Asp	Leu	Glu	Glu	Gln	Lys	195	200	205
Leu	Tyr	Trp	Ala	Asp	Ala	Lys	Leu	Ser	Phe	Ile	His	Arg	Ala	Asn	Leu	210	215	220
Asp	Gly	Ser	Phe	Arg	Gln	Lys	Val	Val	Glu	Gly	Ser	Leu	Thr	His	Pro	225	230	235
Phe	Ala	Leu	Thr	Leu	Ser	Gly	Asp	Thr	Leu	Tyr	Trp	Thr	Asp	Trp	Gln	245	250	255
Thr	Arg	Ser	Ile	His	Ala	Cys	Asn	Lys	Arg	Thr	Gly	Gly	Lys	Arg	Lys	260	265	270
Glu	Ile	Leu	Ser	Ala	Leu	Tyr	Ser	Pro	Met	Asp	Ile	Gln	Val	Leu	Ser	275	280	285
Gln	Glu	Arg	Gln	Pro	Phe	Phe	His	Thr	Arg	Cys	Glu	Glu	Asp	Asn	Gly	290	295	300
Gly	Trp	Ser	His	Leu	Cys	Leu	Leu	Ser	Pro	Ser	Glu	Pro	Phe	Tyr	Thr	305	310	315
Cys	Ala	Cys	Pro	Thr	Gly	Val	Gln	Met	Gln	Asp	Asn	Gly	Arg	Thr	Cys	325	330	335
Lys	Ala	Gly	Ala	Glu	Glu	Val	Leu	Leu	Ala	Arg	Arg	Thr	Asp	Leu		340	345	350
Arg	Arg	Ile	Ser	Leu	Asp	Thr	Pro	Asp	Phe	Thr	Asp	Ile	Val	Leu	Gln	355	360	365
Val	Asp	Asp	Ile	Arg	His	Ala	Ile	Ala	Ile	Asp	Tyr	Asp	Pro	Leu	Glu	370	375	380
Gly	Tyr	Val	Tyr	Trp	Thr	Asp	Asp	Glu	Val	Arg	Ala	Ile	Arg	Arg	Ala	385	390	395
Tyr	Leu	Asp	Gly	Ser	Gly	Ala	Gln	Thr	Leu	Val	Asn	Thr	Glu	Ile	Asn	405	410	415
Asp	Pro	Asp	Gly	Ile	Ala	Val	Asp	Trp	Val	Ala	Arg	Asn	Leu	Tyr	Trp	420	425	430
Thr	Asp	Thr	Gly	Thr	Asp	Arg	Ile	Glu	Val	Thr	Arg	Leu	Asn	Gly	Thr	435	440	445
Ser	Arg	Lys	Ile	Leu	Val	Ser	Glu	Asp	Leu	Asp	Glu	Pro	Arg	Ala	Ile	450	455	460
Ala	Leu	His	Pro	Val	Met	Gly	Leu	Met	Tyr	Trp	Thr	Asp	Trp	Gly	Glu	465	470	475
Asn	Pro	Lys	Ile	Glu	Cys	Ala	Asn	Leu	Asp	Gly	Gln	Glu	Arg	Arg	Val	485	490	495
Leu	Val	Asn	Ala	Ser	Leu	Gly	Trp	Pro	Asn	Gly	Leu	Ala	Leu	Asp	Leu	500	505	510
Gln	Glu	Gly	Lys	Leu	Tyr	Trp	Gly	Asp	Ala	Lys	Thr	Asp	Lys	Ile	Glu	515	520	525
Val	Ile	Asn	Val	Asp	Gly	Thr	Lys	Arg	Arg	Thr	Leu	Leu	Glu	Asp	Lys	530	535	540
Leu	Pro	His	Ile	Phe	Gly	Phe	Thr	Leu	Leu	Gly	Asp	Phe	Ile	Tyr	Trp	545	550	555
Thr	Asp	Trp	Gln	Arg	Arg	Ser	Ile	Glu	Arg	Val	His	Lys	Val	Lys	Ala	565	570	575

Ser	Arg	Asp	Val	Ile	Ile	Asp	Gln	Leu	Pro	Asp	Leu	Met	Gly	Leu	Lys	580	585	590
Ala	Val	Asn	Val	Ala	Lys	Val	Val	Gly	Thr	Asn	Pro	Cys	Ala	Asp	Arg	595	600	605
Asn	Gly	Gly	Cys	Ser	His	Leu	Cys	Phe	Phe	Thr	Pro	His	Ala	Thr	Arg	610	615	620
Cys	Gly	Cys	Pro	Ile	Gly	Leu	Glu	Leu	Leu	Ser	Asp	Met	Lys	Thr	Cys	625	630	635
Ile	Val	Pro	Glu	Ala	Phe	Leu	Val	Phe	Thr	Ser	Arg	Ala	Ala	Ile	His	645	650	655
Arg	Ile	Ser	Leu	Glu	Thr	Asn	Asn	Asn	Asp	Val	Ala	Ile	Pro	Leu	Thr	660	665	670
Gly	Val	Lys	Glu	Ala	Ser	Ala	Leu	Asp	Phe	Asp	Val	Ser	Asn	Asn	His	675	680	685
Ile	Tyr	Trp	Thr	Asp	Val	Ser	Leu	Lys	Asn	Ile	Ser	Arg	Ala	Phe	Met	690	695	700
Asn	Gly	Ser	Ser	Val	Glu	His	Val	Val	Glu	Phe	Gly	Leu	Asp	Tyr	Pro	705	710	715
Glu	Gly	Met	Ala	Val	Asp	Trp	Met	Gly	Lys	Asn	Leu	Tyr	Trp	Ala	Asp	725	730	735
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Gln	Val	Leu	Val	Trp	Arg	Asp	Leu	Asp	Asn	Pro	Arg	Ser	Leu	Ala	Leu	755	760	765
Asp	Pro	Thr	Lys	Gly	Tyr	Ile	Tyr	Trp	Thr	Glu	Trp	Gly	Gly	Lys	Pro	770	775	780
Arg	Ile	Val	Arg	Ala	Phe	Met	Asp	Gly	Thr	Asn	Cys	Met	Thr	Leu	Val	785	790	795
Asp	Lys	Val	Gly	Arg	Ala	Asn	Asp	Leu	Thr	Ile	Asp	Tyr	Ala	Asp	Gln	805	810	815
Arg	Leu	Tyr	Trp	Thr	Asp	Leu	Asp	Thr	Asn	Met	Ile	Glu	Ser	Ser	Asn	820	825	830
Met	Leu	Gly	Gln	Glu	Arg	Val	Val	Ile	Ala	Asp	Asp	Leu	Pro	His	Pro	835	840	845
Phe	Gly	Leu	Thr	Gln	Tyr	Ser	Asp	Tyr	Ile	Tyr	Trp	Thr	Asp	Trp	Asn	850	855	860
Leu	His	Ser	Ile	Glu	Arg	Ala	Asp	Lys	Thr	Ser	Gly	Arg	Asn	Arg	Thr	865	870	875
Leu	Ile	Gln	Gly	His	Leu	Asp	Phe	Val	Met	Asp	Ile	Leu	Val	Phe	His	885	890	895
Ser	Ser	Arg	Gln	Asp	Gly	Leu	Asn	Asp	Cys	Met	His	Asn	Asn	Gly	Gln	900	905	910
Cys	Gly	Gln	Leu	Cys	Leu	Ala	Ile	Pro	Gly	Gly	His	Arg	Cys	Gly	Cys	915	920	925
Ala	Ser	His	Tyr	Thr	Leu	Asp	Pro	Ser	Ser	Arg	Asn	Cys	Ser	Pro	Pro	930	935	940
Thr	Thr	Phe	Leu	Leu	Phe	Ser	Gln	Lys	Ser	Ala	Ile	Ser	Arg	Met	Ile	945	950	955
Pro	Asp	Asp	Gln	His	Ser	Pro	Asp	Leu	Ile	Leu	Pro	Leu	His	Gly	Leu	965	970	975

Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys Phe Ile Tyr
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 Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp Asp Gly Thr
 995 1000 1005
 Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn Pro Asp Arg
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 Tyr Asp Arg Asn His Val Thr Gly Ala Ser Ser Ser Ser Ser Ser
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<220>

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<220>

<223> Artificial sequence is a primer.

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23

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<211> 20

<212> DNA

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<220>

<223> Artificial sequence is a primer.

<400> 14

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<220>
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<210> 24

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<223> Artificial sequence is a primer.

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<223> Artificial sequence is a primer.

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<223> Artificial sequence is a primer.

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<210> 37
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<223> Artificial sequence is a primer.

<400> 37

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<210> 38
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<220>
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<400> 38
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<210> 39
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<220>
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<400> 39
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 <211> 163
 <212> DNA
 <213> Homo sapiens

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 <211> 419
 <212> DNA
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<400> 41
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 agaccaaccg catcgagggt gccaacctca atggcacatc ccggaagggt ctcttctggc 360
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<210> 42
 <211> 221

<212> DNA
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<400> 42
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 ctgaccatcg acctggagga gcagaagctc tactgggctg acgccaagct cagcttcac 180
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 <212> DNA
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 aggtgctgag ccaggagcgg cagccttttt gtgagtgcg g 221

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 <211> 156
 <212> DNA
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<400> 44
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 <212> DNA
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 catccgcagg gcgtacctgg acgggtctgg ggcgcagacg ctggtcaaca ccgagatcaa 240
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 <212> DNA
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ctggccctgg	acctgcagga	ggggaagctc	tactggggag	acgccaagac	agacaagatc	180
gaggtgaggc	tcctgtgg					198

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 <212> DNA
 <213> Homo sapiens

<400> 47						
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gccgcagcat	cgagcgggtg	cacaaggtca	aggccagccg	ggacgtcatc	attgaccagc	180
tgcccgaact	gatggggctc	aaagctgtga	atgtggccaa	ggtcgtcggg	gagtcggggg	240
ggtc						244

<210> 48
 <211> 313
 <212> DNA
 <213> Homo sapiens

<400> 48						
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ggatctccct	cgagaccaat	aacaacgacg	tggccatccc	gctcacgggc	gtcaaggagg	240
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aggtagcgtg	ggc					313

<210> 49
 <211> 255
 <212> DNA
 <213> Homo sapiens

<400> 49						
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gggcccagac	tgggaccaac	agaatcgaag	tggcgcggct	ggacgggcag	ttccggcaag	180
tcctcgtgtg	gagggacttg	gacaacccga	ggtcgctggc	cctggatccc	accaaggggt	240
aagtgtttgc	ctgtc					255

<210> 50
 <211> 210
 <212> DNA
 <213> Homo sapiens

<400> 50						
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ttcatggacg	ggaccaactg	catgacgctg	gtggacaagg	tgggccgggc	caacgacctc	120

accattgact	acgetgacca	gcgcctctac	tggaccgacc	tggacaccaa	catgatcgag	180
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 <212> DNA
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ccgacaagac	tagcggccgg	aaccgcaccc	tcattccagg	ccacctggac	ttcgtgatgg	180
acatcctggg	gttccactcc	tcccgccagg	atggcctcaa	tgactgtatg	cacaacaacg	240
ggcagtgtgg	gcagctgtgc	cttgccatcc	ccggcggcca	ccgctgcggc	tgccctcac	300
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<210> 52
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aaagccatcg	actatgacct	actggacaag	ttcatctact	gggtggatgg	gcgccagaac	180
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 <212> DNA
 <213> Homo sapiens

<400> 53						
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caataccatc	aacgtccaca	ggctgagcgg	ggaagccatg	gggtgggtgc	tgctggggga	180
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<210> 54
 <211> 218
 <212> DNA
 <213> Homo sapiens

<400> 54						
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cgcgcagccc	tggacggcac	cgagcgcgag	gtcctcttca	ccaccggcct	catccgccct	120
gtggccctgg	tggatggaaa	cacactgggc	aagctgttct	gggtggacgc	ggacctgaag	180
cgcattgaga	gctgtgacct	gtcaggtacg	cgccccgg			218

<210> 55

<211> 234
 <212> DNA
 <213> Homo sapiens

<400> 55
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 gcctgaccat ccttggcaag catctctact ggatcgaccg ccagcagcag atgatcgagc 120
 gtgtggagaa gaccaccggg gacaagcgga ctgcgcatcca gggccgtgtc gcccacctca 180
 ctggcatcca tgcagtggag gaagtcagcc tggaggagtt ctgtacgtgg gggc 234

<210> 56
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 <212> DNA
 <213> Homo sapiens

<400> 56
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 ttgccaaggg tgatgggaca ccacggtgct catgcccagt ccacctcgtg ctcttcgaga 120
 acctgctgac ctgtggaggt aggtgtgacc taggtgc 157

<210> 57
 <211> 272
 <212> DNA
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<400> 57
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 <212> DNA
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 tggtagacca gctt 134

<210> 59
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 <212> DNA
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<400> 59
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agctacttcc	atctcttccc	gccccctccg	tccccctgca	cggactcatc	ctgacctcgg	300
ccgggccact	ctggcttctc	tgtgcccctg	taaatagttt	taaatatgaa	caaagaaaaa	360
aatatatatt	atgatttaaa	aaataaatat	aattgggatt	ttaaaaacat	gagaaatgtg	420
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